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TITLE OF INVENTION: ANTIGENED MODILATION OF INPERI
TITLE OF INVENTION: EXPRESSION
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    Isis Pharmaceuticals, Inc.
2292 Faraday Avenue

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COMPUTER: IBM PC compatible
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FILING DATE: June 26, 1998
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COMPUTER READABLE FORM:
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MOLECULES INFLUENCING THE SHEDDING OF THE THE THE RECEPTORS, THEIR PREPARATION AND THEIR USE
                  367 oProLeuArqTrpLysGluPheValArqArqLeuGlyLeuSerAspHisG 384
                                                                                                                                                                                                                                     417 rLeuGluLeuLeuGlyArqValLeuArqAspMetAspLeuLeuGlyCysL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cqn2_6/ptodata/2/ina/5A_COMB.seq:US-08-321-668-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE. Floepy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PATEM: PC-ECOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-CCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-CCT-1993
ATTORNEY/AGNNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BROWDY AND NEITHAGE STREET: 419 Seventh Street, N.W., Suite 300
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08321668
Patent No. 5665859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VARFOLOMEEV, Eugene APPLICANT: BATKIN, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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THILX: 248633
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                 1606 CCCAGTCTTCTCAGA 1620
                                                                                                                                                                                                                                                                                                                                                                                              451 ProSerLeuLeuArg 455
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TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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COMPUTER READARLE FORM:
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NAME/KEY: CDS

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201 AsnValLycdlyThrGlwAspSerGlyThrThrValLeuLeuProleuVa 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 rCysHisAlaGlyPhePheLeuArgCluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 lilePhePheClyLeuCysLeuLeuSerLeuLeuPhelleGlyLeuMetT 234
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                                                                                                                                                                                                                                                                       1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                  34 euGlyAspArgGluLysArgAspSerVal^ysProGlaGlyLysTyrIle 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 67
                                                                                                                                 Percent Identity: 100,000
                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-321-668-1 from: 1 to: 2175
                                                                                                                                                                       alignment_block:
US-09-525-998A-2 x US-08-321-668-1
                                                                                                          Ratio: 5.466
Percent Similarity: 100.000
                                                                                       Quality: 2487,00
Ratio: 5,466
                                                                         alignment_scores:
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US-08-321-668-1
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TITLE OF INVENTION: WOLDOLDS INFORMATINE SHEGGING OF TITLE OF INVENTION: THE RECEPTOR OF THEIR OSE NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSED.
                                                                                                                                                                                                                                                                                                                                                                               1006 ICGAYAAAAAAAAAGGGGAAGCIIGAAAGGAAYIA\IA\IIII 1055
                                                                                                                                      1056 GGCCCCAAACCCAAGCTTCAGTCCCACTTCAGGCTTCACGCCCAACTTG5 1105
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ysalualydaheedladiyihadadhaysedae 267
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                                                                                                                                                                                                                    1306 CIAGACACTGATGACCCGGGGGGGTGTACGCCGTGGTGGAGAACGTGCC
                                                                                                                                                                                                                                                                                      301 ProGlyAspCysProAsnPheAlaPlaProArgArgGluValAlaProPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysFrovinser
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STREET: 419 Seventh Street, N.W., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 1, Application 95/08837941
: Patent No. 5766917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANI: WALLACH, DAVID
APPLICANI: BKAKEBUSCH, COTD
APPLICANI: VARFOLDMERY, Engence
AFLICANI: BAIKIN, Michael
IITLE OF INVENTION: WALFOLDIS: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1606 CCCAGTCTTCTCAGA 1620
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17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 rl.cuTyrAsnAspCysProClyProClyClnAspThrAspCysArgGluC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fersent identity, 100,000
                                                              Patentin Release #1 0 Version #130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 2175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Longth:
                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WASLACH-13
                                                                                                                                                             US 08/321.668
                                                                                             APPLICATION NUMBER: US/OR/837 941
FILING DATE: 28-APR-1997
                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            4BER: 11, 107268
12-001 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-837-941-1
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US-09-525-998A-2 x US-08-837-941-1
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION.
                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                         APPLICATION NUMBER: 11.10
                                                                                                                                                                                                                           ATTORNEY / AGENT INFORMATION:
                 Floppy disk
                                                                                                                                                                                                                                                                                                            202-628-5197
202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                            2175 base pairs
                                                                                                                                                                                                                                              NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2°
                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                SHOURNCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5,466
Percent Similarity, 100,000
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 2487.00
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256..1620
                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
                 MEDIUM TYPE:
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCALION:
                                                               SOFTWARE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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1306 CIAGACACIGATGACCCCGGAAGACTATAGAGGTGC 1355
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                                                                234 yrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGlyLys 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 SerThrProGluLysGluGlyGluLeuGluGlyThrThrThrLysProLe 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 lyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
117 sThrValAspArgAspThrValCysGlyCysArgLysAsuGlnTyrArgH 134
                                                                                                                                        151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 167
                                                                                                                                                                                                            167 rCysHisAlaGlyPheDeLeuArgGluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                                                                184 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
                                                                                                                                                                                                                                                                                                                                                                                                                        906 CATTITCTITGGTCTTIGGCTTTTATCGGTCTTCATTGGTTTAATGT 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 offyrGlnGlyAlaAspProlleEeuAlaThrAlaLeuAlaSerAspProl 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350
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417 rteuGlubeubeuGlyArgValLeuArgAspMetAspLeuDeuGlyCyst. 434

alignment_block:

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EXPRESSION OF THE RECOMBINANT TUMOR NECROSIS FACTOR BINDING PROIEIN 1 (TBP-I)
                 1506 GCTGGAGCTGCTGGAGGCGTGTGCGCACATGAACCTGCTGGAGTGCC 1555
                                                                       434 eugluAspileGluGluAlaLeuCysGlyProAlaAlaLeuProProAla 450
seq_damme: (5 qn?_6/p fod ra, 7) Tray/TA_Y MK seq 98×38 1.2 016-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/126,016
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALLACH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/625668
FILING DATE: 13-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                        Sequence 1, Application US/08126016
Patent No. 5811261
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KEMPER, OLIVER
APPLICANT: BRAKEMENN, HAKTMUT
APPLICANT: HKAKEMESCH, COKD
APPLICANT: ADERKA, DAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-628-5197
TELEPRONE: 202-737-4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2175 base pairs
                                                                                                                                                                                                                                                                                                                WALLACH, DAVID
                                                                                                                                                                                                                                                                                                                               NOPHAR, YARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                 mat_peptide
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000
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                                                                                                                            451 ProSerLeuLeuArg 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                        seq_documentation_block:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-126-016-1
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184 sitCystystystystations from the tystam bystantial incition of a 200 milesty from the first of the first o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ufculeuValGlyfleTyrProSerGlyValfleGlyfeuValProHist 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 euGlyAspArgGinLysAigAspSerVal@ysProGinGlyLysiyille 50
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US-09 525-998A-2 x US-08-125-016-1
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1106 GCIICAAICCCGGGGGCCAAFFCAACIFTACFCAAGCCAAGCAAAAC 1155
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284 lyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
                                                                            301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProPr 317
                                                                                                                                                       317 oTyrGlnGlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProl 334
                                                                                                                                                                                                                                  334 leProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGlnSer 350
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                                                                                                                                                                                                                                                                                                               351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr
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APPLICANT: M.Feldmann, F.W. Gray,
APPLICANT: M.J.C. Truner, F.M. Brennan
IITLE OF INVENTION: Modified human TWFalpha (Tumor
IITLE OF INVENTION: Modified human TWFalpha (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rolease #1.0. vorsion #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.PA.PSP, 176F
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10:May 1993
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08050319B Patent No. 5633145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 Bryant Street
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block
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ATTORNEY/AGENT INFORMATION:

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84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
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    ChartyrAsuAsperystr attyrrattystuAspthrAsptysArquinct 84

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                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identify: 99.780
NAME: ROBBINS, ROBERTA I.,
REGISTRATION NUMBER: 3 ± 208
REFERENCE/DOCKET NUMBER: 5150-0030
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ 1D NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-050-319B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
cs-09-525 996A-2 x US 98 950 3198 24
                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 5.467
Percent Similarity: 99.780
                                                                                                                                                                                                                                                                                                                                                                   Quality: 2482.00
                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 155..1519
                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                      Linear
                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                              US-08-050-319B-24
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STRUKAL INFORMATIONS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 LeuAspThrAspAspPr=AlaThrI==TyrAlaValValGluAsuValPr 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 lulleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1305 AGATCGATCGGTIGGAGTTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAA 1354
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184 snoystystysSertractudysPartystoudysTouProGlaffeCls 200
                                                          317 oTyrdlndlyAlaAspProlleLeuAlaThrAlaLeuAlaSerAspProl 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 TyrserMetLeuAlaThrTrpArqArqArqThrProArqArqGluAlaTh 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 rLeuGluLeuLeuGlyArqValLeuArqAspMetAspLeuLeuGlyCysL 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 lilePhePheGlyLeuCysLeubeuserLeubeuPheIleGlyLeuMetT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 CAITITCITIGGICITIGGCCTTTTATCCCTCCTCTTCATTGGTTTAATCT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    855 ATCOCIACCAACGGGGAAGTCCAAGCTCTACTCCALLGTTGCGGGAAA 904
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Sequence 24, Application US,09465982

seq_documentation_block: ; Patent No. 5863786

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155 ATGGGCCTCTCCCACCGTGCCTGCTGCTGCTGGTGGTGCTGCTGGA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetGlyLouSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuGl 17
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APPLICANI: M.FCIdmann, P.W. Gray,
APPLICANI: M.J.C. Turner, F.M Brennan
IIILE OF INVENTION: Modified human INFalpha (Tamorifile of INVENTION: Nectosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identify: 99.780
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TEERATING STOTIM, PC D.G./MS-DOS
SOFIWARE: Latentin Release #1.0, version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEGISTRATION NUMBER, 33,208
RETERENCE, TC. YET NUMBER: 5150-0030
TELEOMONICALION, INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMBER: 08/08/050,319
10-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35, 194, 807, 20
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US-09-525-998A-z x US 0x 465 982 24
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                                                                                                                                                                                                                                                                                  ADDRESSED: keed & kobbins
STREEL, 635 Bryant Street
CIIY: Palo Alto
STATE: California
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INFORMATION FOR SEQ ID NO: 24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Robbins, Roberta L. REGISTRATION NUMBER: 33,2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICAL ON DATA:
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ADDRESSED: Rood & RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER.
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STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILIRG DATE
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334 leProAssProLeuChilysTrpCluAspScrAlaHisLysProCluSer 356
                                                                                                    101 SerCysSerLysCysArqLysGluMetGlyGlnValGluIleSerSerCy 117
                                                                                                                     117 sThrValAspArdAspThrValCysClyCysArqLysAsnGlnTyrArgH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                       snCystystystysSerf.cuCluCysThrtysLeuCyst.cuProCln:1eclu 200
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355 CITGIACAAIGACIGICCAGGCCCGGGGCAGGAIACGGACIGCAGGGAGI 404
                                84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                                   505 CACAGTGGACCGGGACACGTGTGGCTGCAGGAAGAACCAGTACCGGC 554
                                                                                                                                                                                                                                            134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                              167 rCysHisAlaGlyPhePheLeuArgCluAsnCluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                   905 TOGACACTICAAAAAAAAAGGGGGGCTTIGAAGGAACTACTACTAAGGCCCCT 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 OPTOLeuArgTrpLysCluPheValArgArgLeuGlyLeuSerAspHisG 384
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1305 AGATICGATICGCITIGGAGFITIGFAGAAQQQQCITICQFITIGGQQQQQQQQQQQAA 1354
                                                                                               384 lulleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
                                                                                                                                                      417 rLeuGluLeuLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFIED RECEPTORS THAT CONTINUOUSLY SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5H_COMB scq:US-08-762-308-10
                                                                             TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh
                    OFERATING SYSTEM. PC-DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UTSD:335--1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/224,593 FILLING DATE: 05-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/762,308
09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08762308 Patent No. 5925548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Beutler, Bruce A. APPLICANT: Bazzoni, Flavia M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1956 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: US,
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81 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
21P: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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aliqnment_block:

US-09-525-998A-2 x US-08:762-308-10

Align seq 1/1 to: US-08-762-308-10 from: 1 to: 1956

- - 17 uteuteuValGlyfleTyrProSerClyVallleGlyLeuValProHist 34
- 146 Tercerda Eddear Acarecar eddecede eddecede edden e
- 196 TIGGIGACCGGGAGAGAGGGATAGCTTGTGTCCCCAAGGAAAGTATGTC 245 34 euGlyAspAraGluLysArqAspSerValCysProGlnGlyLysTyrIle 50
 - 51 HisProClnAsnAsnSerlleCysCysThrLysCysHisLysClyThrTy 67
- 296 CTIGGTGAGTGACTGICCGAGGCCGGGGATACAGICTGCAGGGAGT 345 67 rleufyrAsnAspCysProGlyProGlyClnAspThrAspCysArgGluC 84
- 84 ysGluserGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
- 346 CICAAAAGGGCACCTTTTACGGCTTCCCACAATTACCTCAGGCAGTGTCTC 395
- - 117 sthrValAspArgAspthrValCysClyCysArqLysAsnClnTyrArgH 134
- 134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
- 151 AsndiyihrValHisLeuSerCysClnGlulysClnAsnThrValCysTh 167
- 167 rCysHisAlaClyPhelheLeuArgCluAshCluCysValSetCysSerA 184
- 696 GCAAATGTCACAAAACCCCAAGAATCAAGTACTAGGGGTGCTGTGACCCT 745 200 GluAseValiysGlyThrGluAspSerGlymhrThrValLeuLeuDroLe 216
- 796 TGTGCCGATATCCCCGGTGGAGGCCCGAAGTCTACTCCATCATTTCTAGG 845

233 etTyrArgTyrGlbArgTrpLycSerLysLeuTyrSerIleValCysGly 249

- 250 LysSerPhrProClutysClutJyClutauCluClyThrThrThrTysPr 266 AACCC RR3 846 GAICCCGICCCIGICAAAGAG . GAGAAGGCTGGA
- 266 oleu.....AlaProAsnProSerPheSerProThrProGlyPheThrP 281
- 281 LOTHLEGGL) Pheses Revail roses Ses The Phethesersers 297

ATTORNEY, NOENT THE RMALLOWS

984 CCCATCAGGCCCATCTTCGGTCCTAGTAAGIGGCACIICATGCCAGCTGT 1033 1131 GCCCAC...COGCAACGTCCTGAACAATGCA3ACCT1GCGATTCTGTATGC 1177 228 TGGGGCTGAG GAGGAGAATALGAGAGCTGGAAATGGAAGAAGGGGCGC 1277 1328 dececedadadadadadelidaangtadtectestesterttecaada 1377 395 Cyst.euArg31nAlaG1n1yrSerMetLeuAlathrirpArgArg1h 411 411 rProArgArgGluAlaThrLeuGluLeuGlyArgValLeuAraAspM 428 378 euGlyLeuSerAspHisGluIleAspArqLeuGluLeuGluAsuGlyArq 594 428 etAspLeuLeuGlyCysLeuGluAsplleGluGluAlaLeuCysGlyPro 444 METHOL FOR SELECTING HIGH-EXPRESSING HOSE CPEUS | FEFFE | FEFF 345 AlaHislysProGluSerLeuAspIbrAspAspProAlaThrieuTyrAL 298 ThrlyrThrProClyAspCysPro.....AscPheAlaAlaProAr 311 gArgGluValAlaProProTyrGlnGlyAlaAspFroIleLeuAlaThrA 361 aValValGluAsnValProProLeuArqTrpLysGluEieVaiArdL 1034 CAGTGAGGLAMPSCCAACC...CAGGGAGCTGACGTGTGTGTGTACGAAT 328 laLeuAlaSerAspProlleProAsnProLeuGlnLySTrpGluAspSer 5.25 inch, 460 Kb floppy disk Seq_hame. ['10,' f, j, j, j, j, j, j, j,]. Mr --- j 's CURRENT APPLICATION DATA: APPLICATION WHERE THE PROPERTY WHERE WAS A SECOND OF THE PROPERTY OF AUDRESSEE: Generiech, Inc.
STREET 460 Point San Bruns Bled
City: South Sar Francisco
STATE: Calification COMPUTER: THE FC compatible OPERATING SYSTEM: PC-DGS/MS-DGS Ecquence 2, Application 95/08286740 Patent No. 5541053 patin (Genentech) Prowley, Craig W. 05 - AUG-1994 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 APPLICATION NUMBER: FILING DATE: NUMBER OF SECUENCES: TROUGHT OF TAVENTRY TITLE OF INVENTION: seq_documentation_block: GENFFAL INFOEMATION: APPLICANI: Crowley USA FILING DATE: 94080 1428 GCC 1430 445 Ala 445 COUNTRY: Patent No.

	AME: Lee, Wendy M. PGISTUATION NIMHED+
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Align s	e4 1/1 to. U
1605	MetGlyLeuSerThrValProAspLeuLeuLeuLeuDeuValLeuLeuGl 17
17	
1655	TEGETGGAATATACCCTCAGGGTTATTGGAACTGGTCCTC
34	euGlyAspArgGluLysArqAspSerValCysProGlsGlyClysTyrIle 50
51	HISProGlamanAshSerlleCysCysThrLysCysHisLysGlyThrTy 67
67	ystroclytroclycl
84	PhethrAlaSerGluAshHisteuArqHistys
101	3EysGluMetGlyGla
117	STB:VALASPATGASPTHTVALCYSCTYCYSARGLYSASHCTHTYFAFGH 134
134	hec Total
151 2055	AsndlythrValHisteuserdysGlndlutysGlnAsnthrValdysTh 167
167	rdyshisaladiyPhePheLeuArgGluAshGluCysValSerCysSerA 184
184	SDCysLysLysEvsSerLeadludysThrLysLeadysEeuProclaffeGta 200

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355 2510	ASP. ProAlaThrLeuTyrAlaValValGluAsnValProP 	368 2559
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seq_name	CTUS COMB seq.PCT-US95-0957	na G
opples	Ξ.	5 Z

COMPUTER REACABLE FORM: COMPUTER REACABLE FORM: MEDIUM TYPE: 5.25 incm: 360 Kb floppy disk COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible OPERATIOS SYSTEM: PC-105S/MS-DOS SOFTWARE: Patin (Generated) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/USG5/09576 FILING DATE: OPERATION: PRIOR APPLICATION NUMBER: PCT/USG5/09576 FILING DATE: OS AUG-1944 ATTORNEY/AGENT INFORMATION: NAME: Lee, Wendy M: NAME: Lee, Wendy M: FRETERENCE/DOCKET NUMBER: 798PCT TELEOMMUNICATION NUMBER: 798PCT TELEOMMUNICATION NUMBER: 798PCT TELEX: 910/371-7168 TELEX: 415/952-9881 TELEX: 415/952-9881 TELEX: 415/952-9881 TELEX: QUICATION POR SEQ: 10 NO: 2: SEQUENCE: CHARACTERISTICS: LINGTH: 6889 bases LINGTH: 6889 bases TENGTH: OPERATION INFORMATION: TOPPLICATION FOR SEQ. 10 NO: 2: SEQUENCE: CHARACTERISTICS: TENGTH: DIRECT CALLING STRANDEDNESS: double TOPPLICATION TOPPLICATIO	_scores:	Ebook: s-daRA-2 x port-magn-hagsze-2 d 1/1 to: Port-US95-09576-2 from: 1 to: 6889	MetalylouserthrValProAsploutoutoutouveluovalLoutoud1 17 	uLeuleuValGlyIleTyrProSerGlyValIleGlyLeuValProHist 34 	euglyasparggluLycArgAspScrValCysProGluGlyLysTyrIle 50 	HisproglnasnasnserilecyscysthriyscysHislysclythriy 67 HITHITHIHHHHHHHHHHHHHHHHHHHHHHHHHHHH CACCECAAAAIAAHEGAHHGGIBLACCAASIGCACAAAGSAACTA 1804	rLeufyrAsnAspCysProdlyProdlyGlaAspThrAspCysArgGluc 84 	yschusorshysorphothralasorchuashisteuarquissysteu 100 	SerCysSerLysCysArglysGluMetGlyGlmValGluHeSerSerCy 117 	ofhrvaldspargdopfhrvalcysGlyGysArgLysAsnGlofyrArgH 134 HTH HTH HTH HTH HTH HTH HTH HTH HTH HT	v
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167	PCYSHISALARI YPhoPhoLeuArdShuAsaGhdCysVal SerGysSerA 	184 2154
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201	ASBVATLYSCLYTERCTBASPSOYCTYTERTEVATLOGICGBYGGLCGYVATLUTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHTHT	217
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312	: AAALCHIGHGACA ACHICCOL "ALDGOLACGGLOCO" ASAGO OLAAALC : gGloValAlabrokre.TyrdloGlyAlaAnpfrelleLegAlalbr	327
2402	::::::	
328 2434	AlaLenAtaSetAspProlleProAsnProLenGIndyStrpGinAsp	
344	SerAlaHistySProGInSersplbtAsp 	
355 2510	- Asp. ProAlaThrLeutyrAlaValValGluAsuValProP 	158 2559
368 2560	roledangtrplysclubbevalatdatgledngtyledseraspHisSlu 	484 2582
385 2593	The Asparational Intend Intend Instance	400
400	00 nTyrserMelleu.AlaThrIrpArdArdArdInrPro 41z 	
Seg_hallie	$(-\beta)^{2} \log \ln^{2} \mathcal{L}(\frac{1}{4})^{-1} \log a_{1}^{2} \mathcal{L}(\frac{1}{4}) \log b_{1}^{2} \mathcal{L}(\frac{1}{4}) \log b_{2}^{2} \mathcal{L}(\frac{1}{4}) \log b_{1}^{2} \mathcal{L}(\frac{1}{4}) \log b_{2}^{2} \mathcal{L}(\frac{1}{4}) \log b_{2$	
sea docum	mentation block:	

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985 GCTGITGGIGGGAATATACCCTCAGGGTTATTGGAGTGGTGCTCAGGC 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetGlyLeuSerfhrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
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                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ITITLE OF INVENTION: SCREENING DRUG LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASCED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OB/627,171A
FILING DATE: 03-APE-1996
                                                                                                                                                                                                                     3: Gen-Probe Incorporated
10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB1016
Sequence 6, Application US/08627151A
Patent No. 5866341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-525-998A-2-x-US-08-627-151A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fisher, Carlos A
REGISTRATION NUMBER: 36,510
                                                             APPLICANT: SPINELLA, Dominic
APPLICANT: BECHERER, Kathleen
APPLICANT: BROWN, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                              1BM Compatible
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TELEFAX: 619-410-8928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6896 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHOUGHOR CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            Diskette
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Ratio: 5.649
Percent Similarity: 100.000
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PRIOR APPLICATION DATA:
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                                                                                                                                                                         NUMBER OF SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                San Diego
                                           GENERAL INFORMATION:
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US-08-627-151A-6
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                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                            STREET
                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                  CITY
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                    Patent No.
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1135 CHTGTACAATGACTGTFCCAGGCCGGGCAGGATACGGAGTGCAGGGAGT 1184
                                         84 ysGluSerGlySerPheThrAlaSerGluAsuHisLeuArdHisCysLeu 100
                                                                                                                             101 SerCysSerLysCysArgLysGluMetGlyGinValGluffeSerSerCy 117
                                                                                                                                                                                                            117 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
                                                                                                                                                                                                                                                                                           134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 rCysHisAlaGlyPhePheLeuArgSluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-050-319B-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1535 AATGTTAAGGGCACTTGAGGACTCAGGCACCACA 1567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 47, Application US/08050319H
; Patent No. 5633145
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 515
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 617-8999
TELEFAX. (415) 327-3231
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed & Robbins
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1: 435
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LENGTH: 600 base pairs
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEGLUM LYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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double

67 rl.cuTyrAsnAspCysProClyProClyClnAspThrAspCysArgGluC 84 us-09-525-998a-2.rni

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201 CTISTACAAIGACTGTCCAGGCCCGGGGGGAAAAAAAAAGGAAGGAGGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40] AFTATTGGAGTGAAAACCTTTTGCAGTGCTTCAATTGCAGCCTCTGGCTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GCIGIIGGIGGGAATATACHTTAGGGGIIAIIGGAATAGTGATTAATA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ysCluScrCiySortharharlaratinalananHistorAngHisrysten 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 CICAGAGGGGCTGGTTGAGGGCTTGAGAAAAGGAGTGGTGAGAGTGGGTTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 SerCysSerLysCysArqLysGluMetGlyGlnValGluIleSerSerCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 sThrVaiAspArgAspThrVaiCysGlyCysArgLysAsnGlnTyrArgH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AsnGlyThrValHisLeuSerCysGlnCluLysGlnAsnThrValCysTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                             51 HisProGlnAsnAsnSerIleCysCycThrLysCysHisLysGlyThrTy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rheuTyrAsnAspCysProClyProClyClnAspThrAspCysArgCluC 84
                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 ut.cuf.cuValCtyfleTyrProSerCtyVallIcGtyLcuValProHist, 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 snCystystysSerieuGluCysThrLysLeuCysLeuProGlnIle 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq_busser //htp2_6/jdindatu_2//htm/fR_MoNR seq-Ms-AR 465-982-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identaty: 99.497
                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-u50-3198-47 from: 1 to: 600
                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application HS/ABA65982; Patent No. 5863786; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: M.Feldmann, P.W. Gray,
                                                                                                                                                                                                                                                                                          alignment_block:
US 09 525-998A 2 x US 08 050 319B 47
                       MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                        Ratio: 5.677
Percent Similarity: 99.497
                                                                                                                                                                                                   Quality: 1124.00
                                                                                      1..597
linear
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                                                                 NAME/KEY: CDS
                                                                                                         US-08-020-319B-47
                                                                                                                                                                                alignment_scores:
ToPology:
                                                                                         1.0CA110N:
                                            FEATURE
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51 GCTGTTGGTGGGAAIAIACCCCTCAGGGGTIA11GGACTGGTCCCTCACC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 TAGGGGACAGGGAGAGAGAGATAGTGTGTGTGTGGAGAAAATATATG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 CACCCTCAAATAATTCGATTTGCTGTACCAAGIGCCACAAAGGAACCTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 euGlyAspAraCluLysAraAspSerValCysProGluGlyLysTyrIle 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 HisProGluAsnAsnSerlleCysCysThrLysCysHisLysGlyThrTy 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 unculouValGlylleTyrProSerGlyValileC:yLeaValProHist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl
APPLICANT: M.J.C. Turner, F.M Brennan
IITLE OF INVENTION: Modified human INFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
COMPRESPONDENCES: 57
COMPRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 99.497
                                                                                                                                                                                                                                                                                                                       SOFTWAME: Patentln Kelease #1.0, version #1.25
CURRINI APPLICATION DATA:
AFFLICATION ROWER. UNJUS,465,982
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-465-982 47 from: 1 to: 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION ROWHIN, 03/08/050.419
FILING DARE, 10 May-1993
AITORNEY/AGENT INPORMATION:
NAME: Robbins, Roberta L.
                                                                                                                                                                                                                                                                                                     GPURALING SYSTEM, IN DAS/MS-1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPRENTIVE FELL MORHER: 5150
THECOMMUNICATION INFORMATION:
THELEFAX: (415) 427-423
INFORMATION FOR SECIED B., 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alidoment_block:
US-09-525-998A-2 x US-08-465-982-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33,208
                                                                                                                                                                                                                                                                                     IBM PC Compatible
                                                                                                             Reed & Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CONA to mENA
                                                                                                 ADDRESSED: Reed a management of 35 Bryant Street
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 600 base pairs
TYPE: nuc.eic acid
STRANDEBHISS: double
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 59.497
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                                                                                                                               SIREET: 635 Bryo
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                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCALION:
US-08-465-982-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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84 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                       251 GTGAGAGGGGCTCTTCACGCTTCAGAAAAACGACGTGAGAGAGTGCGCCC 300
                                                                               101 SerCysSerLysCysArqLysGluMetGlyGlnValGluIleSerSerCy 117
                                                                                                   117 SThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 134
                                                                                                                                                                                                                                                     134 isTyrTrpSerGluAsmLeuPheGlnCysPheAsmCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                                           151 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 167
                                                                                                                                                                                                                                                                                                                                                          167 rCysHisAlaGlyPhePheLeuArqGluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                              184 snCystystysSerieuCluCysThrLysteuCysteuProCinile 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq.name: /rqn2_6/ptodata/2/ina/Kk_rhMB seq.us-08-804-166-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/804,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMPRELL-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYBRID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER, IHM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/011.936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
   Sequence 7, Application US/08804166
   Patent No. 6193972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BROWDY AND NEIMAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE CHOCKET NUMBER CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 628-5197
TELLEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1301 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chappel FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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169 isAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerAsnCys 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 CAAGAGGGCAGTGCCGATAGTGTGTCCCCAAGGAAAAATATATGCACCC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 SerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCy 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 sSerLysCysArqLysGluMetGlyGlnValGluIleSerSerCysThrV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530 CYCCAAATGCCGAAAAGGAAATGGGYCAGGYGGAGAYCYCTTGYTGYTGCAGA 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 alAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHlsTyr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TripSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeuAsnGl 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 yThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysThrCysH 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730 ATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCTCTGTAGTAACTGT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 GCCCCATCATGCACCCTGGCTGTGAAAAAAAGAAGAATGCCCTGTGTGTC 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 ValleuseuProLeuValIlePhePheCtyLeuGys....culeuSeric 227
                                                                                                                                                                                                                                                                                                                                                    3 LeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuLe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                         19 uValGlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 octaAsaAsaSerIleOysOysThrLysOysHisLysOlyThrTyrLeuT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 yrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluCysGlu 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 tystysSerteuGluCysThrtysLeuCyst.euProGlnifeGluAsnVa
                                                                                                                                               Length: 384
Gaps: 12
Percent Identity: 54.948
                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-U8-804-166-7 from: 1 to: 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 llysGlyThrGluAspSerGlyThrThr......
                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US 09 525 998A:2 x US-08-804-166-7
                                                                                                                                               Quality: 1016.00
Ratio: 3.923
                                                                                                                                                                                             67.448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z99 ..... GGTTTTTGGTTGGT
                                         279..1287
                    CDS
                                                                                                                                                                                         Percent Similarity:
                                     ; LOCATION:
US-08-804-166-7
                                                                                                                                 aliqnment_scores:
                    NAME/KEY:
FEATURE:
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930 AICACCGICAACAGCAGCAGGGGGGGGGGGGGGGGGGGG	::: :::111 111 ::::::::::::::::::::	aLembelledlyteamettyrArgtyrdla.ArgtrpLysSerLysLeu 243 	FyrSerHeValCySClyt/gaSerThrProClut/gsCluC)yClut.caG; 260	JAShProSerPheSerPrefi 	roGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPhe 293 :::	- 6 - 4	okrjakigoluvalalahroprotyrcinciyalaasperoticicualat 327 	hralaLeualaseraspProTleProAsnProTeuGlntysTrpGluAsp 343 	SerAlaHistysProGinSericaAspThrAspAspProAla 357 H
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102 sScriys/ysarqtys/luwctd/ys/tu/letes/srs/ys/krv 119
| HTHTHTH | HTHTHTHTHTH; CHITET; L. C. FILL
| 5:0 GP/DAACTTTAAASAAATTTTASHGSASAETCTTGAAAS 779
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TELEPHONE: (202) 628-5197
| INLEPAM: (202) 737 3528
| INFORMATION FOR SEQ ID NO: 7:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 1301 base pairs
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STRANDEDNESS: single
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US-08-910-991-7
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419 Seventh Street N.W., Ste. 300
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APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/804,166
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Patent No. 6193972
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1027
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SerClySerPheThrAlaSerCluAsnHisLeuArgHisCysLeuSerCy 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 alAspArqAspThrValCysGlyCysArqLysAsnGlnTyrArqHisTyr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TrpSerGluAsnLeuPheGluCysPheAsnCysSerLeuCysLeuAsnGl 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 ....cachminadechadh.....aradechadannaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 TCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTACTTGT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 (SA)adly Fibeth-CanArgil (AshributysVallegar), s2etA, 67ys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 i.euSerThrValFroAspleuheuheuProLeuValheuheuGluheuhe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 uValGlyIleTyrFroSerGlyValIleGlyLeuValProHisLeuGlyA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 yrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluCysGlu 85
                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 83.871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-U8-8U4-166-5 from: 1 to: 1147
                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                  REFERENCE/DOCKET NUMBER: CAMPBELL-2A TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 February 1996
                                                 NAME: Browdy, Roger D. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-525-998A 2 x US-08-804-166-5
                                                                                                                    TELEPHONE: (202) 628-5197
TELEFAX: (202) 737 3528
INFORMATION FOR SEQ ID NO: 5:
                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1147 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                     5.131
89.401
                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     995.50
                                                                                                                                                                                                                                                                                                                 278..1132
                                                                                                                                                                                                                                                             MOLECULE TYPE: CONA
                                                                                                                                                                                                                                             Linear
FILING DATE: 20
                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio.
                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-804-166-5
                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                  FEATURE:
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- 729 ATGCAGGTITCLLFCTAGAGAAAACGAGTGTCTCCTCTAGTAACTGT 778

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